

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number:

10/585,503

Source:

THOR

Date Processed by STIC:

7/19/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 07/19/2006

PATENT APPLICATION: US/10/585,503

TIME: 08:22:58

Input Set : A:\265.00450101.ST25.txt

Output Set: N:\CRF4\07192006\J585503.raw

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3 <110> APPLICANT: Hamill, Owen P.
4      Maroto, Rosario
6 <120> TITLE OF INVENTION: MECHANOSENSITIVE ION CHANNELS AND METHODS OF USE
8 <130> FILE REFERENCE: 265.00450101
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/585,503
C--> 10 <141> CURRENT FILING DATE: 2006-07-07
10 <150> PRIOR APPLICATION NUMBER: 60/535,327
11 <151> PRIOR FILING DATE: 2004-01-09
13 <150> PRIOR APPLICATION NUMBER: PCT/US2005/000722
14 <151> PRIOR FILING DATE: 2005-01-10
16 <160> NUMBER OF SEQ ID NOS: 7
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 35
22 <212> TYPE: PRT
23 <213> ORGANISM: Artificial
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Channel blocker GsMTx-4 (Grammostola spatulata venom 4 kDa
27      peptide)
29 <400> SEQUENCE: 1
31 Gly Cys Leu Glu Phe Trp Trp Lys Cys Asn Pro Asn Asp Asp Lys Cys
32 1      5      10      15
35 Cys Arg Pro Lys Leu Lys Cys Ser Lys Leu Phe Lys Leu Cys Asn Phe
36      20      25      30
39 Ser Ser Gly
40      35
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 759
45 <212> TYPE: PRT
46 <213> ORGANISM: Homo sapiens
48 <400> SEQUENCE: 2
50 Met Met Ala Ala Leu Tyr Pro Ser Thr Asp Leu Ser Gly Ala Ser Ser
51 1      5      10      15
54 Ser Ser Leu Pro Ser Ser Pro Ser Ser Ser Ser Pro Asn Glu Val Met
55      20      25      30
58 Ala Leu Lys Asp Val Arg Glu Val Lys Glu Glu Asn Thr Leu Asn Glu
59      35      40      45
62 Lys Leu Phe Leu Leu Ala Cys Asp Lys Gly Asp Tyr Tyr Met Val Lys
63 50      55      60
66 Lys Ile Leu Glu Glu Asn Ser Ser Gly Asp Leu Asn Ile Asn Cys Val
67 65      70      75      80
70 Asp Val Leu Gly Arg Asn Ala Val Thr Ile Thr Ile Glu Asn Glu Asn
71      85      90      95

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74 Leu Asp Ile Leu Gln Leu Leu Leu Asp Tyr Gly Cys Gln Lys Leu Met
75           100           105           110
78 Glu Arg Ile Gln Asn Pro Glu Tyr Ser Thr Thr Met Asp Val Ala Pro
79           115           120           125
82 Val Ile Leu Ala Ala His Arg Asn Asn Tyr Glu Ile Leu Thr Met Leu
83           130           135           140
86 Leu Lys Gln Asp Val Ser Leu Pro Lys Pro His Ala Val Gly Cys Glu
87 145           150           155           160
90 Cys Thr Leu Cys Ser Ala Lys Asn Lys Lys Asp Ser Leu Arg His Ser
91           165           170           175
94 Arg Phe Arg Leu Asp Ile Tyr Arg Cys Leu Ala Ser Pro Ala Leu Ile
95           180           185           190
98 Met Leu Thr Glu Glu Asp Pro Ile Leu Arg Ala Phe Glu Leu Ser Ala
99           195           200           205
102 Asp Leu Lys Glu Leu Ser Leu Val Glu Val Glu Phe Arg Asn Asp Tyr
103           210           215           220
106 Glu Glu Leu Ala Arg Gln Cys Lys Met Phe Ala Lys Asp Leu Leu Ala
107 225           230           235           240
110 Gln Ala Arg Asn Ser Arg Glu Leu Glu Val Ile Leu Asn His Thr Ser
111           245           250           255
114 Ser Asp Glu Pro Leu Asp Lys Arg Gly Leu Leu Glu Glu Arg Met Asn
115           260           265           270
118 Leu Ser Arg Leu Lys Leu Ala Ile Lys Tyr Asn Gln Lys Glu Phe Val
119           275           280           285
122 Ser Gln Ser Asn Cys Gln Gln Phe Leu Asn Thr Val Trp Phe Gly Gln
123           290           295           300
126 Met Ser Gly Tyr Arg Arg Lys Pro Thr Cys Lys Lys Ile Met Thr Val
127 305           310           315           320
130 Leu Thr Val Gly Ile Phe Trp Pro Val Leu Ser Leu Cys Tyr Leu Ile
131           325           330           335
134 Ala Pro Lys Ser Gln Phe Gly Arg Ile Ile His Thr Pro Phe Met Lys
135           340           345           350
138 Phe Ile Ile His Gly Ala Ser Tyr Phe Thr Phe Leu Leu Leu Leu Asn
139           355           360           365
142 Leu Tyr Ser Leu Val Tyr Asn Glu Asp Lys Lys Asn Thr Met Gly Pro
143           370           375           380
146 Ala Leu Glu Arg Ile Asp Tyr Leu Leu Ile Leu Trp Ile Ile Gly Met
147 385           390           395           400
150 Ile Trp Ser Asp Ile Lys Arg Leu Trp Tyr Glu Gly Leu Glu Asp Phe
151           405           410           415
154 Leu Glu Glu Ser Arg Asn Gln Leu Ser Phe Val Met Asn Ser Leu Tyr
155           420           425           430
158 Leu Ala Thr Phe Ala Leu Lys Val Val Ala His Asn Lys Phe His Asp
159           435           440           445
162 Phe Ala Asp Arg Lys Asp Trp Asp Ala Phe His Pro Thr Leu Val Ala
163           450           455           460
166 Glu Gly Leu Phe Ala Phe Ala Asn Val Leu Ser Tyr Leu Arg Leu Phe
167 465           470           475           480
170 Phe Met Tyr Thr Thr Ser Ser Ile Leu Gly Pro Leu Gln Ile Ser Met

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[illegible]

242 <210> SEO ID NO: 3

243 <211> LENGTH: 4085

244 <212> TYPE: DNA

245 <213> ORGANISM: Homo sapiens

247 <400> SEQUENCE: 3

248	ccgggcctcg	agccgaggca	gcagtgggaa	cgactcatcc	tttttccagc	cctggggcgt	60
250	ggctggggtc	ggggtcgggg	tcggggccgg	tgggggcccc	gccccgtct	cctggcctgc	120
252	ccccttcattg	ggccgcgatg	atggcgcccc	tgtaccgcag	cacggacctc	tcggggcgct	180
254	cctcctcctc	cctgccttcc	tctccatcct	cttcctcgcc	gaacgagggtg	atggcgctga	240
256	aggatgtgcg	ggagggtgaag	gaggagaata	cgctgaatga	gaagcttttc	ttgctggcgt	300
258	gcgacaaggg	tgactattat	atggttaaaa	agattttgga	ggaaaacagt	tcagggtgact	360
260	tgaacataaaa	ttgcgtagat	gtgcttgggg	gaaatgctgt	taccataact	attgaaaacg	420
262	aaaacttgga	tatactgcag	cttcttttgg	actacggttg	tcagaaacta	atggaacgaa	480
264	ttcagaatcc	tgaqtattca	acaactatgg	atgttcaccc	tgtcattttta	gctgctcatc	540

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266	gtaacaacta	tgaaattctt	acaatgctct	taaaacagga	tgtatctcta	cccaagcccc	600
268	atgcagttgg	ctgtgaatgc	acatttgtgt	ctgcaaaaaa	caaaaaggat	agcctccggc	660
270	attccaggtt	tcgtcttgat	atatatcgat	gtttggccag	tccagctcta	ataatgttaa	720
272	cagaggagga	tccaattctg	agagcatttg	aacttagtgc	tgatttaaaa	gaactaagtc	780
274	ttgtggaggt	ggaattcagg	aatgattatg	aggaaactagc	ccggcaatgt	aaaatgtttg	840
276	ctaaggattt	acttgcacaa	gcccgggaatt	ctcgtgaatt	ggaagttatt	ctaaaccata	900
278	cgtctagtga	cgagcctctt	gacaaacggg	gattattaga	agaaagaatg	aattttaagtc	960
280	gtctaaaact	tgctatcaaa	tataaccaga	aagagtttgt	ctcccagctc	aactgccagc	1020
282	agttcctgaa	cactgttttg	tttggacaga	tgtcrggtta	ccgacgcaag	cccacctgta	1080
284	agaagataat	gactgttttg	acagtaggca	tcttttgccc	agttttgtca	ctttgttatt	1140
286	tgatagctcc	caaattctcag	tttggcagaa	tcattcacac	accttttatg	aaatttatca	1200
288	ttcatggagc	atcatatttc	acatttctgc	tgttgcttaa	tctatactct	cttgtctaca	1260
290	atgaggataa	gaaaaacaca	atggggccag	cccttgaaag	aatagactat	cttcttattc	1320
292	tgtggattat	tgggatgatt	tggtcagaca	ttaaaagact	ctgggatgaa	gggttggaa	1380
294	actttttaga	agaattcgt	aatcaactca	gttttgtcat	gaattctctt	tatttggcaa	1440
296	cctttgccct	caaagtgggt	gtcacaaca	agtttccatg	ttttgctgat	cggaaggatt	1500
298	gggatgcatt	ccatcctaca	ctgggtggcag	aagggctttt	tgcatttgca	aatgttctaa	1560
300	gttatcttcg	tctctttttt	atgtatacaa	ccagctctat	cttgggtcca	ttacagattt	1620
302	caatgggaca	gatgtttaca	gattttggaa	aatttcttgg	gatgtttctt	cttgttttgt	1680
304	tttctttcac	aattggactg	acacaactgt	atgataaagg	atatacttca	aaggagcaga	1740
306	aggactgtgt	aggcatcttc	tgtgaacagc	aaagcaatga	taccttccat	tcgttcattg	1800
308	gcacctgctt	tgctttgttc	tggtatattt	tctccttagc	gcatgtggca	atctttgtca	1860
310	caagatttag	ctatggagaa	gaactgcagt	cccttgtggg	agctgtcatt	gttggtagat	1920
312	acaatgtcgt	ggttgtgatt	gtgcttacca	aactgctggg	ggcaatgctt	cataaaagct	1980
314	ttcagttgat	agcaaatcat	gaagacaaa	aatggaagtt	tgctcgagca	aaattatggc	2040
316	ttagctactt	tgatgacaaa	tgtacgttac	ctccaccttt	caacatcatt	ccctcaccaa	2100
318	agactatctg	ctatatgatt	agtagcctca	gtaagtggat	ttgctctcat	acatcaaaag	2160
320	gcaaggtcaa	acggcaaaac	agtttaaaag	aatggagaaa	tttgaaacag	aagagagatg	2220
322	aaaactatca	aaaagtgatg	tgctgcctag	tgcatcgtaa	cttgacttcc	atgagacaga	2280
324	agatgcaaat	tacagatcag	gcaactgttg	aaaactaaa	cgaactgcgc	caagatctgt	2340
326	caaaattccg	aaatgaaata	agggattttc	ttggctttcg	gacttctaaa	tatgctatgt	2400
328	tttatccaag	aaattaaacca	ttttctaaat	catggagcga	ataattttca	ataacagatc	2460
330	caaaagacta	tattgcataa	cttgcaatga	aattaatgag	atatatatgt	aaataaagaa	2520
332	ttatgtaaaa	gccattcttt	aaaatatatta	tagcataaat	atatgttatg	taaagtgtgt	2580
334	atatagaatt	agttttttta	accttctgtt	agtggctttt	tgcagaagca	aaacagatta	2640
336	agtagataga	ttttgttagc	atgctgcttg	gttttcttac	ttagtgtctt	aaaatgtttt	2700
338	tttttatgtt	taagaggggc	agttataaat	ggacacattg	cccagaatgt	tttgtaaaat	2760
340	gaagaccagc	aaatgtaggc	tgatctcctt	cacaggatac	acttgaaata	tagaagttat	2820
342	gttttaata	tctctgtttt	aggagttcac	atatagttca	gcatttatgt	tttaggagta	2880
344	taattttatt	ttatctaaaa	taatagtcta	tttttctttt	tgtattttgt	tataatctta	2940
346	agcaacaaa	aaaaaacctt	aatattttgaa	tctattttatg	tctttcaatt	taaattcact	3000
348	tcagtttttg	ttattgtaat	atattttactt	ttacatgggt	ataatcactt	tatattttta	3060
350	atgttttttt	cacttaatat	tttatatata	catttccatg	tattgatgta	gttagtccac	3120
352	atttaaaatt	ttatagaatt	atatagtttt	tgaaaaatac	agtcagtaga	tgttttattt	3180
354	tttagctatt	cagttatgtt	tataagtttg	catagctact	tctcgacatt	tggtttgttt	3240
356	taattttttt	gtatcataat	agtcctattt	ttttttcaag	ttggagtga	tgtttttagt	3300
358	tttaagatag	ataggagaca	cttttttattc	acatgtagtc	acaacctgtt	ttgttttgtt	3360
360	aaaacatagg	aagtctcttt	aatgcaatga	tttgttttat	atttggacta	aggttcttga	3420
362	gcttatctcc	caagggtactt	tccataattt	aacacagctt	ctataaaagt	gacttcatgc	3480

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Input Set : A:\265.00450101.ST25.txt

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364 ttacttgtgg atcattcttg ctgcttaaga tgaaaagcat tggtttttta aaattagaga 3540
366 ataaaaatat tatttaaatt tttggtgtgt tcacataaag ggatgtagct aaaatgtttt 3600
368 cataggctat tatatatctt cgcagcattt ccagttaaga ggatattagg tatataattc 3660
370 tcttcttaac cgaatgtcag atggtcttac gccacaggtt gcaggtaacc cttggtctgt 3720
372 aagcaccacc gatccaggga tcattgtcta aataggttac tattgtttgt ttcattctgc 3780
374 ttttgcattt ttatttttta atttccaaat ttttaagtgt ccctctttgg ggcaaattct 3840
376 tataaaaatg tttattgtaa agttatatat tttgtctacg atgggattat gcacttccca 3900
378 attgggattt tacatctgga tttttagtca ttctaaaaaa cacctaatta ttaaaacatt 3960
380 tatagagtgc ctactgtatg catgagttga gttgcttctg aggtacattt tgaatgacag 4020
382 catattgtaa gaaaaaaaaa ggtgaataaa atttgacatt agattataaa aaaaaaagg 4080
384 aattc 4085

387 <210> SEQ ID NO: 4
388 <211> LENGTH: 30
389 <212> TYPE: DNA
390 <213> ORGANISM: Artificial
392 <220> FEATURE:
393 <223> OTHER INFORMATION: Scrambled antisense oligonucleotide
395 <400> SEQUENCE: 4
396 cttttgaccg ctcattcccta tagtatttgc 30
399 <210> SEQ ID NO: 5
400 <211> LENGTH: 12
401 <212> TYPE: PRT
402 <213> ORGANISM: Artificial
404 <220> FEATURE:
405 <223> OTHER INFORMATION: Epitope of MscCa polypeptide
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409 Cys Val Gly Ile Phe Cys Glu Gln Gln Ser Asn Asp
410 1 5 10
413 <210> SEQ ID NO: 6
414 <211> LENGTH: 15
415 <212> TYPE: PRT
416 <213> ORGANISM: Artificial
418 <220> FEATURE:
419 <223> OTHER INFORMATION: Epitope of MscCa polypeptide
421 <400> SEQUENCE: 6
423 Gln Leu Tyr Asp Lys Gly Tyr Thr Ser Lys Glu Gln Lys Asp Cys
424 1 5 10 15
427 <210> SEQ ID NO: 7
428 <211> LENGTH: 31
429 <212> TYPE: PRT
430 <213> ORGANISM: Artificial
432 <220> FEATURE:
433 <223> OTHER INFORMATION: Channel blocker GsMTx-1
435 <400> SEQUENCE: 7
437 Tyr Cys Gln Lys Trp Met Trp Thr Cys Asp Glu Glu Arg Lys Cys Cys
438 1 5 10 15
441 Glu Gly Leu Val Cys Arg Leu Trp Cys Lys Lys Lys Ile Glu Trp
442 20 25 30

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/585,503

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Input Set : A:\265.00450101.ST25.txt  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,4,5,6,7

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/585,503

DATE: 07/19/2006

TIME: 08:22:59

Input Set : A:\265.00450101.ST25.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date